Lukas Heumos

Curriculum Vitae

2018–2020	Master of Science Bioinformatics, Eberhard Karls Universität Tübingen, Tübingen, 1.37 - ongoing.
2015–2018	Bachelor of Science Bioinformatics, Eberhard Karls Universität Tübingen, Tübingen, 1.79 .
	Masters's Thesis
Title	GPU reproducible end-to-end machine learning
Supervisors	Dr. Sven Nahnsen (Director Quantitative Center for Biology), Professor Dr. Philipp Hennig (Max Plank Institute for Intelligent Systems, University of Tübingen)
Description	Investigation of GPU based determinism of major machine learning frameworks and development of a best practices framework based on mlflow. In progress.
	Experience
	Activities
01.11.2019– 01.11.2020	iGEM Tübingen Advisor , <i>Tübingen</i> . Advising the iGEM Team Tübingen, project development, teaching bioinformatics and software engineering.
28.06.2020-	Lindau Nobel Online Science Days, Virtual.
01.07.2020	Talks and discussions with nobel laureates.
	Lindau Nobel Sciathon, Virtual.
	Examining similarities and differences between the COVID-19 pandemic and climate change.
	COVID-19 Virtual Biohackathon , ONLINE. SEIR modelling of COVID-19 infections; discriminating feature detection across different SARS-Cov2 sequences; nf-core coordinator for gene expression based global infection analysis
	Hackzurich, ETH Zürich, VIRTUAL.
30.03.2020	Agent-based modelling of COVID-19 infections in Switzerland
	nf-core hackathon, Francis Crick Institute London. End-to-end machine learning with nextflow and proteomics nextflow pipelines
	$\begin{tabular}{ll} \textbf{AI hackathon}, \ HELMHOLTZ \ AI \ MUNICH. \\ Machine learning for improved cancer differential diagnosis by multi-level MALDI imaging molecular-morphological data \\ \end{tabular}$

Education

iGEM Tübingen team member , TÜBINGEN. Team leading, finance (raised more than 15000€), web development, bacterial RNA-Seq data analysis, metabolic modelling and development of a machine learning based cell-penetrating peptide efficacy predictor.
$\label{eq:core_norm} \textbf{nf-core hackathon}, \ T\ddot{\textbf{U}} \\ \textbf{BINGEN}. \\ \\ \textbf{Implementation of Nextflow pipelines for label-free proteomics data and GUIDE-Seq data}. \\$
$\label{eq:GEMTUBINGEN} \begin{tabular}{ll} \textbf{iGEM Tübingen team member}, $T\ddot{\textbf{U}}BINGEN. \\ Homology modelling, molecular dynamics simulations, development of a machine learning based deimmunization workflow. \\ \hline \textbf{Vocational} \\ \end{tabular}$
Software Developer and Scientific Support, QUANTITATIVE BIOLOGY CENTER (QBIC), Tübingen. Software development of libraries, tools and portlets. Design and development of a containerized large-scale machine learning infrastructure based on Apache Spark. GUIDE-Seq data analysis.
TOEFL Test Administrator and Team Leader, TOEFL TEAM TÜBINGEN, Tübingen. Leading the student based TOEFL Team Tübingen and supervising TOEFL tests.
Systems Administrator and Scientific Support, Paleogenetics Group of Prof. Dr. Dr. Verena Schünemann, Tübingen. Maintained the computational infrastructure and provided scientific bioinformatics support.
Teaching Teaching Assistant for Biomedical Data Management Seminar, UNIVERSITY OF TÜBINGEN, QUANTITATIVE BIOLOGY CENTER, Tübingen

- Supervising master students in a seminar about commercial clouds in biomedical research.
- 03.09.2019— Bioinformatics and Lab Course, EXPERIMENTA SCIENCE CENTER, Heilbronn. 06.09.2019 Introduced DNA, sequencing, CRISPR-Cas9, bioinformatics, project development and management with applied sessions to high school students.

Awards and Honors

- 2020 Nominated by the University of Tübingen to attend the interdisciplinary 70th Lindau (postponed to Nobel Laureate Meeting and accepted by the Lindau Meeting Council 2021)
 - 2019 Invited by New England Biolabs to meet Nobel Laureate Richard J. Roberts in Ipswich, USA
 - 2019 iGEM bronze medal for iGEM Team Tübingen 2019
 - 2019 Bestowed 'Award for Exceptional Student Commitment for iGEM Tübingen' by the University of Tübingen
 - 2018 iGEM silver medal for iGEM Team Tübingen 2018
 - 2015-2019 e-fellows scholarship
 - 2015 9th out of more than 1000 teams in German Founders' Prize for Students competition
 - 2014-2016 Professional Starcraft 2 player

Kapellenweg 27 – 72070 Tübingen lukasheumos.com

Computer skills

Basic R, Bash, Apache Spark, Singularity

Intermediate LATEX, WEB DEVELOPMENT, MACHINE LEARNING, DOCKER, C++, MLFLOW

Advanced PYTHON, NEXTFLOW, JAVA, LINUX

Talks

10.2019 On 'GLP.exe' (iGEM Tübingen project 2019) in Boston, USA, at the Giant Jamboree

04.2015 About 'Gloready' (German Founders' Prize for Students project) in Stuttgart and Hamburg at the Landesbank Baden-Württemberg Sparkasse and the grand finals

Languages

German Mothertongue

English Fluent

French Intermediate

Publications

- Lamsfus-Calle*, A., A. Daniel-Moreno, G. Urena, J. Rottenberger, J. Raju, T. Epting, S. Marciano, L. Heumos, P. Baskaran, J. S. Antony, R. Handgretinger, and M. Mezger. "Universal gene correction approaches for β-hemoglobinopathies using CRISPR/Cas9 and AAV6 donor template delivery". In: Submitted (2020)
- Lamsfus-Calle, A., A. Daniel-Moreno, J. S. Antony, T. Epting, L. Heumos, P. Baskaran, J. Admard, N. Casadei, N. Latifi, D. M. Siegmund, M. S. D. Kormann, R. Handgretinger, and M. Mezger. "Comparative targeting analysis of KLF1, BCL11A, and HBG1/2 in CD34+ HSPCs by CRISPR/Cas9 for the induction of fetal hemoglobin". In: Scientific Reports 10.1 (June 2020), p. 10133. ISSN: 2045-2322. DOI: 10.1038/s41598-020-66309-x. URL: https://doi.org/10.1038/s41598-020-66309-x
- 3. Ferrarini, M., V. Aguiar-Pulido, E. T. Dawson, A. Guarracino, A. Gruber, **L. Heumos**, A. Kanitz, A. Lal, B. E. Pickett, R. Rebollo, and et al. "Global analysis of human SARS-CoV-2 infection and host-virus interaction". In: *BioHackrXiv* (May 2020). DOI: 10.37044/osf.io/b4zkp. URL: biohackrxiv.org/b4zkp
- 4. Ballesio, F., A. H. Bangash, D. Barradas-Bautista, J. Barton, A. Guarracino, **L. Heumos**, A. Panoli, M. Pietrosanto, A. Togkousidis, P. Davis, and et al. "Determining a novel feature-space for SARS-CoV-2 sequence data". In: *BioHackrXiv* (May 2020). DOI: 10.37044/osf.io/xt7gw. URL: biohackrxiv.org/xt7gw
- Bichmann, L., A. Nelde, M. Ghosh, L. Heumos, C. Mohr, A. Peltzer, L. Kuchenbecker, T. Sachsenberg, J. S. Walz, S. Stevanović, H.-G. Rammensee, and O. Kohlbacher. "MHCquant: Automated and Reproducible Data Analysis for Immunopeptidomics". In: Journal of Proteome Research 18.11 (2019). PMID: 31589052, pp. 3876—3884. DOI: 10.1021/acs.jproteome.9b00313. eprint: https://doi.org/10.1021/acs.jproteome.9b00313. URL: https://doi.org/10.1021/acs.jproteome.9b00313

Kapellenweg 27 – 72070 Tübingen

(a) +49 (176) 92633135 • □ lukas.heumos@posteo.net

(b) lukasheumos.com

6. Widerspick, L., L. Heumos, B. Nowack, and A. Abbasi. "Junge Molekularbiologie-Teams kreieren faszinierende Innovationen". In: *BIOspektrum* 25.7 (2019), pp. 796–797. ISSN: 1868-6249. DOI: 10.1007/s12268-019-1092-0. URL: https://doi.org/10.1007/s12268-019-1092-0